

GenCore version 5.1.4-p5 4578
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protein - protein search, using sw model

run on: May 19, 2003, 16:36:02 ; Search time 15.7956 Seconds
 (without alignments)
 982.052 Million cell updates/sec

title: US-09-625-573-2
 perfect score: 1970
 sequence: 1 MLSTSRSFIRNTNESGEEV..... .GRGKSTIGRAPEASLQDKEGA 374
 scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

searched: 112892 seqs, 41476328 residues
 total number of hits satisfying chosen parameters: 112892

post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

database: SwissProt_40.4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Query Score	Match	Length	DB ID	Description
1	1970	100.0	374	1 CKR2_HUMAN	P41597 homo sapi
2	1614.5	82.0	360	1 CKR2_MACMU	018793 macaca mu
3	1346.5	68.4	373	1 CKR2_RAT	051693 rattus no
4	1332.4	67.6	373	1 CKR2_MOUSE	051683 mus muscu
5	1244	63.1	354	1 CKR5_MOUSE	P51682 macaca mu
6	1236	62.7	352	1 CKR5_CERTO	062243 cercopith
7	1236	62.7	352	1 CKR5_HYDLE	097883 hylobates
8	1230	62.4	352	1 CKR5_MACMU	P51686 macaca mu
9	1230	62.4	352	1 CKR5_PANTR	P51644 pan trogl
10	1230	62.4	352	1 CKR5_PONY	097881 pongo pyg
11	1230	62.4	354	1 CKR5_RAT	001556 rattus no
12	1228	62.3	352	1 CKR5_GORGO	P56439 gorilla g
13	1228	62.3	352	1 CKR5_PAPHA	P56441 papio ham
14	1224	62.1	352	1 CKR5_HUMAN	P15181 homo sapi
15	1224	62.1	352	1 CKR5_PYGBE	097882 pygathrix
16	1223	62.1	352	1 CKR5_PYGBI	097880 pygathrix
17	1223	62.1	352	1 CKR5_TRAFR	097878 trachypit
18	1223	62.1	352	1 CKR5_TRAPR	097779 trachypit
19	1211	61.5	352	1 CKR5_CERAE	P56493 cercopith
20	967.5	49.1	355	1 CKR1_HUMAN	P32246 homo sapi
21	951.5	48.3	359	1 CKR3_MOUSE	P51278 mus muscu
22	945	48.0	359	1 CKR3_RAT	054814 rattus no
23	931.5	47.3	358	1 CKR3_CAVPO	092213 cavia por
24	911.5	46.3	355	1 CKR1_MACMU	P56482 macaca mu
25	899.5	45.7	355	1 CKR1_MOUSE	P51675 mus muscu
26	886.5	45.0	355	1 CKR2_MACMU	P56483 macaca mu
27	876	44.5	355	1 CKR2_MACMU	P56492 cercopith
28	867	44.0	355	1 CKR3_CERAE	P51680 mus muscu
29	833	42.3	360	1 CKR4_MOUSE	P51679 homo sapi
30	831.5	42.2	360	1 CKR4_HUMAN	P51676 mus muscu
31	731	37.1	356	1 CKR7_MOUSE	P51677 homo sapi
32	723	36.7	355	1 CKR8_MACMU	097665 macaca mu
33	715	36.6	355	1 CKR8_MACMU	097666 macaca mu

RESULT 1					
CKR2_HUMAN			STANDARD;		
ID	CKR2_HUMAN	AA.	PRT;	374 AA.	
34	708.5	36.0	353	1	CKR8_MOUSE
35	704.5	35.8	354	1	C3XL_RAT
36	698	35.4	355	1	C3X1_HUMAN
37	692	35.1	354	1	C3X1_MOUSE
38	588	29.8	384	1	CKD6_HUMAN
39	584	29.6	378	1	CKR7_MOUSE
40	580	29.4	378	1	CKD6_MOUSE
41	575.5	29.2	378	1	CKR7_RAT
42	575	29.2	382	1	CKD6_RAT
43	569	28.9	357	1	CKR9_HUMAN
44	564	28.6	367	1	CKR6_MOUSE
45	563	28.6	369	1	CKR9_MOUSE
P56484 mus musculu					
P35411 rattus norv					
P19238 homo sapien					
Q92999 mus musculu					
Q00590 homo sapien					
P32248 homo sapien					
Q08107 mus musculu					
P47774 mus musculu					
P49027 rattus norv					
P51686 homo sapien					
Q56489 mus musculu					
Q9WQT7 mus musculu					
ALIGNMENTS					
[1]					
SEQUENCE FROM N.A.					
RP MEDLINE:94198821; PubMed=8146186;					
RA Charo I.F.; Myers S.J.; Herman A.; Franci C.; Connolly A.J.;					
RA Coughlin S.R.;					
RT "Molecular cloning and functional expression of two monocyte					
RT chemoattractant protein 1 receptors reveals alternative splicing of					
RT the carboxy-terminal tails.";					
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).					
[2]					
SEQUENCE FROM N.A.					
RP MEDLINE:94324942; PubMed=8048929;					
RA Yamagami S.; Tokuda Y.; Ishii K.; Tamaka H.; Endo N.;					
RA "cDNA cloning and functional expression of the human monocyte					
RT chemoattractant protein 1 receptor gene. Evidence for the role of the					
RT carboxy-terminal tail in receptor trafficking.";					
RL Biophys. Res. Commun. 202:1156-1162(1994).					
[3]					
SEQUENCE FROM N.A.					
RP MEDLINE:97150864; PubMed=8995400;					
RA Wong L.-M.; Myers S.J.; Tsou C.-L.; Gosling J.; Arai H.; Charo I.F.;					
RT "Organization and differential expression of the human monocyte					
RT chemoattractant protein 1 receptor gene. Evidence for the role of the					
RT carboxy-terminal tail in receptor trafficking.";					
RL J. Biol. Chem. 272:1038-1045(1997).					
[4]					
SEQUENCE FROM N.A.					
RP McCombie W.R.; Wilson R.; Chen E.; Gibbs R.; Zuo L.; Johnson D.;					
RA Nhan M.; Parneil L.; Dedia N.; Ansari A.; Mardis E.; Schutz K.;					
RA Gnoj L.; Ia Bastide M.; Kaplan N.; Greco T.; Touchman J.;					
RA Muzyk D.; Chen C.N.; Evans C.; Fitzgerald M.; See L.H.; Tang M.;					
RT "Organization and differential expression of the human monocyte					
RT chemoattractant protein 1 receptor gene. Evidence for the role of the					
RT carboxy-terminal tail in receptor trafficking.";					
RL Biophys. Res. Commun. 202:1156-1162(1994).					
[5]					
SEQUENCE FROM N.A.					
RP MEDLINE:20501139; PubMed=11046064;					
RX Porec B.M.; Dragan Y.; Giacalone J.; Pae A.; Powell E.;					
RA Chakravarty L.; Kolattukudy P.E.;					
RA "Monocyte chemoattractant protein-1 receptor CCR2B is a glycoprotein that					
RT has tyrosine sulfation in a conserved extracellular N-terminal region.";					

FT	TRANSMEM	207	226	5 (POTENTIAL).				
FT	DOMAIN	227	243	CYTOSMATIC (POTENTIAL).				
FT	TRANSMEM	244	268	6 (POTENTIAL).				
FT	DOMAIN	269	285	EXTRACELLULAR (POTENTIAL).				
FT	TRANSMEM	286	309	7 (POTENTIAL).				
FT	DOMAIN	310	360	CYTOSMATIC (POTENTIAL).				
FT	CARBHYD	14	14	N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	MOD_RES	26	26	SULFATE (BY SIMILARITY).				
FT	DISULFIDE	112	190	BY SIMILARITY.				
SQ	SEQUENCE	360 AA;	41139 MW;	4B252BC5913F89F CRC64;				
Query Match		82.0%	Score 1614.5;	DB 1;	Length 360;			
Best Local Similarity		96.6%	Pred. No. 3.1e-93;					
Matches		308;	Conservative 4;	Mismatches 3;	Gaps 1;			
QY	1	MLSTSRSRIFRNTNSGEVTTFFDYDGA PCKHDVKQGAQOLLPLPLSVLFTFGVGN	60					
Db	1	MLSTSRSRIFRNTNSGEVTTFFDYDGA PCKHDVKQGAQOLLPLPLSVLFTFGVGN	60					
QY	61	MLVVLILINCKKLKLTDTYLNLAISDLFLITPL WMAHSAANDWVGNAMCKLFTGLY	120					
Db	61	MLVVLILINCKKLKLTDTYLNLAISDLFLITPL WMAHSAANDWVGNAMCKLFTGLY	120					
QY	121	HIGYFGGIGFFLILIDRYLAIHVAFKLA RTVTEGVTGVTSVITWLVAVASVPLIFTK	180					
Db	121	HIGYFGGIGFFLILIDRYLAIHVAFKLA RTVTEGVTGVTSVITWLVAVASVPLIFTK	180					
QY	181	CQEDSVYVCGPYFPQGNWNFHTMNLGVL PLIMIVCYSGILKTLKLRCRNEKKHR	240					
Db	181	CQEDSVYVCGPYFPQGNWNFHTMNLGVL PLIMIVCYSGILKTLKLRCRNEKKHR	240					
QY	241	AVRVIPTIMIVYFLFPTVNVVILNT QEFQFGLSNCESTSQLDQATQVETLGMT HCCI	300					
Db	241	AVRVIPTIMIVYFLFPTVNVVILNT QEFQFGLSNCESTSQLDQATQVETLGMT HCCI	300					
QY	301	NPITYAFGEKFR--SLF	316					
Db	301	NPITYAFGEKFRYLSMF	319					
RESULT 3								
CKR2-RAT								
ID	CKR2-RAT							
AC	Q55193;							
DT	16-OCT-2001 (Rel. 40, Created)							
DT	16-OCT-2001 (Rel. 40, Last sequence update)							
DE	C-C chemokine receptor type 2 (C-C CKR-2) (CCR2).							
EN	Rat2 or CMFBR2.							
OS	Rattus norvegicus (Rat).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthellia; Rodentia; Sciurognathus; Muridae; Murinae; Rattus.							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN-Sprague-Dawley;							
RX	MEDLINE-98318173; PubMed-9655467;							
RA	Jiang Y., Salairana M.N., Adhikari S., Xia Y., Feng L., Sonnag M.K., defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.,							
RT	"Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyelitis (EAE) has been induced.							
RL	J. Neuroimmunol. 86:1-12(1998).							
CC	-!- FUNCTION-RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5 CHEOKINNS TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL (BY SIMILARITY).							
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.							
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND MACROPHAGES.							
CC	-!- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.							
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.							
CC	--!- This SWISS-PROT entry is copyright. It is produced through a collaboration							
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=96205938; PubMed=8631787;
 RA Boring L., Gosling J., Montecclaro F.S., Lusis A.J., Tsou C.-L.,
 RA Charo I.F.;
 RT "Molecular cloning and functional expression of murine JE (monocyte
 chemoattractant protein 1) and murine macrophage inflammatory protein
 1alpha receptors: evidence for two closely linked C-C chemokine
 receptors on chromosome 9";
 RT J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=96216044; PubMed=8662823;
 RA Kurihara T., Bravo R.;
 RT "Cloning and functional expression of mCCR2, a murine receptor for
 the C-C chemokines JE and FIC."
 RT J. Biol. Chem. 271:11603-11606(1996).
 RN [3]
 SEQUENCE FROM N.A.
 RX MEDLINE=97026720; PubMed=8872898;
 RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
 RA Post T.W., Gerard C., Dorf M.E.;
 RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
 transcriptase-polymerase chain reaction does not detect mRNA for the
 KC or new MCP-1 receptor";
 RT J. Neurosci. Res. 45:382-391(1996).
 CC "-I- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
 CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CALCIUM IONS LEVEL.
 CC "-I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC "-I- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
 BUT NOT IN NONHEMATOPOIETIC CELL LINES.
 CC "-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@issb-sib.ch).
 CC -----
 DR EMBL; AAC52453; 1.
 DR EMBL; U56179; AAC52557; 1.
 DR MGI; MGI:106185; Cmbr2.
 DR InterPro; IPIR000276; GPCR_Rhoopsn.
 DR PRINTS; PR00237; GPCR_RHOOPSN.
 DR PROSITE; PS00271; G_PROTEIN_RECEP_F1-1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1-2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 56 83 1 (POTENTIAL).
 FT DOMAIN 84 93 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 94 114 2 (POTENTIAL).
 FT DOMAIN 115 127 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 128 149 3 (POTENTIAL).
 FT DOMAIN 150 166 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 167 191 4 (POTENTIAL).
 FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 220 239 5 (POTENTIAL).
 FT DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 257 281 6 (POTENTIAL).
 FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 299 322 7 (POTENTIAL).
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISFIELD 126 203 BY SIMILARITY.
 FT CONFLICT 39 39 Y -> H (IN REF. 1).
 FT CONFLICT 184 184 A -> G (IN REF. 1).

FT CONFLICT 264 264 Score 1332.5; DB 1; Length 373;
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C325A CRC64;

 Query Match 67.6%; Score 1332.5; DB 1;
 Best Local Similarity 76.3%; Pred. No. 8e-76;
 Matches 255; Conservative 26; Mismatches 46; Indels 7; Gaps 3;

 Qy 1 MLSTSRSRFIRNTNNSGEBRVEITFDDYDGYAPCHKFQDQGAQFLPLAPPLYSLVFIFGVCN 60
 Db 14 ILSLTSFLSFLTRSIQELGATTPYDIDGEPCKTTSVQIGAWLPLPSLVEIFGVCN 73

 Qy 61 MLVVLILINCKKLKCLTDIYLNLAISDPLFLITPLWAHSAAANEWFGNAMCKLFTGLY 120
 Db 74 MLVVLILIGCKRLKSMIDYLNLAISDPLFLITPLWAHYAAANEWFGNIMCKVFTGLY 133

 Qy 121 HIGYFGIGIFFLILTDRLYLAVHAFALKARTVTVGIVTSVTLVAVFASVPGIIFTK 180
 Db 134 HIGYFGIGIFFLILTDRLYLAVHAFALKARTVTVGIVTSVTLVAVFASVPGIIFTK 193

 Qy 181 CQKEDSVYVCGYFPRGWNHFTIMMRNLGLVPLLIMVICYSGIILKTLRCRNEKKHR 240
 Db 194 SKQDDHYTCGPYFTQWLKNQTIMMNLSSLPLMWICYSGLHTLFLRCRNEKKHR 253

 Qy 241 AVRVTITIMVYFLFPTPYNIVLNTFQEFGLSNCESTSOLDQATQVTEFLGMTHGCI 300
 Db 254 AVRVTIAIMVYFLFPTPYNIVLFLTQESLGMSNCVDKHLDQANQVTEFLGMTHGCI 313

 Qy 301 NPITYAFVGEEFR--SLF--HIALG-CRIAPL 327
 Db 314 NPVIAFVGEEFRYLSIFFRKHIAKRLCKQCPV 347

 RESULT 5
 CRR5_MOUSE
 ID CRR5_MOUSE STANDARD; PRT; 354 AA.
 AC P51632; Q61867; P97005; Q35313; P97308; Q3891;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CRR-5) (CCR-5) (MIP-1
 DE alpha receptor).
 GN CCR5 OR CMKBR5
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muriae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ; TISSUE=Spine;
 RX MEDLINE=96205938; PubMed=8631787;
 RA Boring L., Gosling J., Montecclaro F.S., Lusis A.J., Tsou C.-L.,
 RA Charo I.F.;
 RA "Molecular cloning and functional expression of murine JE (monocyte
 RT Chemoattractant protein 1) and murine macrophage inflammatory protein
 RT 1alpha receptors: evidence for two closely linked C-C chemokine
 RT receptors on chromosome 9.";
 RL J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=96278910; PubMed=8662890;
 RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.,
 RA "Cloning and characterization of a novel murine macrophage
 RT inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 271:14445-14451(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Ola;
 RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Liver, Kidney, and Spleen;

RX	MEDLINE=98001387; PubMed=9343222;
RA	Kubmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RA	"Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses.;"
RT	"Two distinct CCR5 domains can mediate coreceptor usage by human immunodeficiency virus type 1.;"
RT	J. Virol. 71:3642-3656(1997).
RL	[5]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE=129;
RA	STRAIN=129;
RC	RX MEDLINE=97404635; PubMed=9261347;
RA	Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Shartron M., Cen Y.H., Domz R.W., Peiper S.C.;
RA	"Wing Z.X., Guo H.H., Du J.G., Accavitti M.A.,
RA	"Two distinct CCR5 domains can mediate coreceptor usage by human immunodeficiency virus type 1.;"
RT	J. Virol. 71:6305-6314(1997).
RL	[6]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE=129;
RA	Guo B., Kuno K., Harada A., Matsushima K.;
RC	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: RECEPTOR FOR A C-3' TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES, BUT NOT IN NONHEMATOPOIETIC CELL LINES.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announcements.html or send an email to license@isb-sib.ch).
CC	CC
DR	EMBL; U47036; AAC5244.1; -.
DR	EMBL; X94151; CAA63867.1; -.
DR	EMBL; U68565; AAB3723.1; -.
DR	EMBL; U83322; AAC53386.1; -.
DR	EMBL; AF022990; AAC53389.1; -.
DR	EMBL; AF019772; AAB71183.1; -.
DR	EMBL; D83648; BAA12024.1; -.
DR	EMBL; MG1:107182; Chikudate.
DR	Intertow; TPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1.1.
DR	PRINTS; PR00237; GPCR_RHODOPSIN
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1-1; 1.
DR	PROSITE; PS00262; G-PROTEIN RECEP_F1_2; 1.
DR	G protein coupled receptor, Transmembrane, Glycoprotein, Polymorphism DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 33 60 EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 71 91 2 (POTENTIAL).
FT	DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 105 126 3 (POTENTIAL).
DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 144 168 4 (POTENTIAL).
FT	DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 201 220 5 (POTENTIAL).
FT	DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 238 262 6 (POTENTIAL).
DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 280 303 7 (POTENTIAL).
FT	DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 103 180 BY SIMILARITY.
FT	CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT 11 11 1 -> S.
FT	VARIANT 62 62 K -> R.
FT	VARIANT 66 66 V -> M.
FT	VARIANT 97 97 I -> V.
FT	VARIANT 109 109 V -> L.
FT	VARIANT 156 156 V -> A.
FT	VARIANT 160 160 F -> S.

Query Match		Score 1244; DB 1; Length 354;	
Best Local Similarity 75.3%; Predicted No. 2.2e-70;		Mismatches 41; Indels 6; Gaps 2;	
Matches 232; Conservative			
Qy	17 GEEVTFFFDYDG--APCHKFIDVKOIGAQLPLPLSIVTFEGFVNMLVLVILINCKLK 74		
Db	5 GSVPTIYDIDGMSAQPKQINVQIAAQPLPLSIVTFEGFVNMMVFLILISCKLK 64		
Qy	75 CLTDIYLLNLAISDLFLPLTPLWAHSAAANEWFGNAMCKLFTGHLTYFGGIFTIIL 134		
Db	65 SVTDIYLLNLAISDLFLPLTLPWAHYANEWFGNIMCKVFTEVYHIGFGGIFTIIL 124		
Qy	135 TIDRYLAIVHAFAALKARTVTFGVVTSVITWLVAVASWPGIIFTKCKEDSVYVCPYF 194		
Db	125 TIDRYLAIVHAFAALKARTVNFQVITSVVTVWVAVAFASLPEIITRSQKEFHHTCSPIF 184		
Qy	195 PRG---WNNFHTIMRNILGLVPLLIVWTCYSGILKTLRCNEKKAHRVRYIFTIMI 250		
Db	185 PHTQYHWWKSFQTLKMYTSLPLLYMTCYSGITLTLRCNEKKAHRVRLIAIMI 244		
Qy	251 YVFLFWTPYNTVILLNTFQEFFGLSNCESTSOLQATOVTETLGTMTHCCINPTIYAFVGE 310		
Db	245 YVFLFWTPYNTVILLTFQEFFGLNCCSSNRLDAMQATELGTMTHCCLNPIYAFVGE 304		
Qy	311 KFRSLFLFH 318		
Db	305 KFRSYLSV 312		
RESULT 6			
CCR5_CERTO	SEQUENCE FROM N.A.		
ID	CPKB5_CERTO	STANDARD:	352 AA.
AC	062743; 062744; 062745; 062746;		
RR	15-DEC-1998 (Rel. 37, Created)		
RA	Chen Z., Gettie A., Ho D.D., Marx P.A.;		
RT	"Primary SIVm isolates use the CCR5 coreceptor from sooty mangabey naturally infected in west Africa: a comparison of coreceptor usage of primary SIVm, HIV-2 and SIVmac." (CCR5).		
RT	CCR5 OR CMKBR5.		
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;		
OC	Cercopithecinae; Cercocetus.		
OX	NCB1_TaxID=9531;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
STRAIN	Isolate 079, 085, 087, and 089;		
RR	STRAIN=Isolate 079; PubMed=9656999;		
RA	Chen Z., Gettie A., Ho D.D., Marx P.A.;		
RT	"Primary SIVm isolates use the CCR5 coreceptor from sooty mangabey naturally infected in west Africa: a comparison of coreceptor usage of primary SIVm, HIV-2 and SIVmac." (CCR5).		
RT	Virology 246:113-124 (1998).		
RL	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	CC		

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RESULT 7	
CRR5_HYLL	
ID	CRR5_HYLL STANDARD; PRT; 352 AA.
AC	097883; AC_097883;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	C-C chemokine receptor type 5 (C-C CRR-5) (CCR5) (CCR5).
GN	CRR5 OR CMKBR5.
OS	Hylobates leucogenys (White-cheeked gibbon)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX	NCBI_TaxID=61853; OX_NCBI_TaxID=61853;
RN	[1]
RP	SEQUENCE FROM N.A. PubMed=10486970;
RX	Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RA	Sequence evolution of the CCR5 chemokine receptor gene in primates. ;
RT	RT Mol. Biol. Evol. 16:1145-1154 (1999).
RL	[1]
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MCP-1-ALPHA, MCP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	[1]
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	[1]
CC	CC EMBL; AF074451; AAD18863_1; -
CC	CC InterPro; IPR00276; GPCR_Rhodopsin.
CC	CC PFAM; PF00001; 7tm_1; 1.
CC	CC PROSITE; PRO0237; GPCR_RHODOPSIN.
CC	CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC	CC PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
CC	CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; DOMAIN_1 30 EXTRACELLULAR (POTENTIAL).
CC	CC FT TRANSMEM 1 30 EXTRACELLULAR (POTENTIAL).
CC	CC FT TRANSMEM 1 301 277 (POTENTIAL).
CC	CC FT TRANSMEM 1 302 278 (POTENTIAL).
CC	CC FT DISULFID 101 302 352 CYTOPLASMIC (POTENTIAL).
CC	CC FT DOMAIN 125 142 178 (POTENTIAL).
CC	CC FT DOMAIN 167 198 (POTENTIAL).
CC	CC FT TRANSMEM 199 218 (POTENTIAL).
CC	CC FT DOMAIN 219 235 (POTENTIAL).
CC	CC FT TRANSMEM 236 260 (POTENTIAL).
CC	CC FT DOMAIN 261 277 (POTENTIAL).
CC	CC FT TRANSMEM 278 301 (POTENTIAL).
CC	CC FT DOMAIN 302 352 (POTENTIAL).
CC	CC FT DISULFID 101 302 352 CYTOPLASMIC (POTENTIAL).
CC	CC FT MOD_RES 3 3 BY SIMILARITY. SULFATION (BY SIMILARITY).
CC	CC FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
CC	CC FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
CC	CC FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
CC	CC FT VARIANT 2 2 D > E (IN ISOLATE 087).
CC	CC FT VARIANT 3 3 Y > D (IN ISOLATE 079).
CC	CC FT VARIANT 25 25 V > G (IN ISOLATE 087).
CC	CC FT VARIANT 100 100 M > N (IN ISOLATE 079).
CC	CC FT VARIANT 107 107 L > V (IN ISOLATE 089).
CC	CC FT VARIANT 134 134 V > G (IN ISOLATE 079).
CC	CC FT VARIANT 146 146 V > L (IN ISOLATES 085 AND 089).
CC	CC FT VARIANT 340 340 T > I (IN ISOLATE 079).
CC	CC SQ SEQUENCE 352 AA; 40489 MW; 20A1962D47E49CA CRC64;
Query Match	62.7%; Score 1236; DB 1; Length 352;
Best Local Similarity	77.3%; Pred. No. 6..9e-30;
Matches	238; Conservative 26; Mismatches 32; Indels 12; Gaps 3;
Cy	24 FDYD-GAPPHKFDVKQIGAQLLPLPLVSYLVEIFGVNMVLVLLINCKLKCLTDYL 81
Db	10 YDIDYTSEPOQKINVQIARLLPLPLVSYLVEIFGVNMVLVLLINCKLKCLTDYL 69
Qy	82 LNLAISDLFLITPLWAHSAANEWVFGNAMCKLFTGLYHIGYEGGFFFLLTIDRYLA 141
Db	70 LNLAISDLFLITPLVFWAHYAAQNDFGNTMCQLLGLYFGFFSGFFFLLTIDRYLA 129
Qy	142 IWHAFALKARTTCTVYVTTWVAYFASVPGTIFTKCGKEDSVYVCGYFP---RG 197
Db	130 IWHAFALKARTTCTVWVAVFASLPGTITRSCREGLYTCSCSHFPYSQYQF 189
Qy	198 WNNFHFTIMRNLLGLVPLLIMVICYSGLKLTLLRCNEKKHRARVIFTMIVYFLWT 257
Db	190 WKNFOTKLIVLGLVPLLIVWVICYSGLKLTLLRCNEKKHRARVIFTMIVYFLWA 249
Qy	258 PYNIVLLNTFQFETGLSNESTSOLOQATVTEPLGMHCINPITYAYGEKERSLF- 316
Db	250 PYNIVLLNTFQFGLNNCSNRLQAMQVTEPLGMTCINPIYYAFGEKFRNLL 309
Qy	317 ----HIA 319
Db	310 VFFQKHIA 317
Query Match	62.7%; Score 1236; DB 1; Length 352;
Best Local Similarity	77.4%; Pred. No. 6..9e-30;
Matches	236; Conservative 25; Mismatches 34; Indels 10; Gaps 2;
OY	25 DYDGA[PCKFEDVQIGAQLLPLPLVSYLVEIFGVNMVLVLLINCKLKCLTDYLNL 84
Db	13 DYDSEPCOKINVQIARLLPLVFWAHYAAQNDFGNTMCQLLGLYFGFFSGFFFLLTIDRYLA 22

QY 85 AISDLPLITPLWAHSANENVFGNAMCKLFTGLYHJGYFGGIFLFLITDRYLAVH 144
 DB 73 AISDLPLITPLWAHSANENVFGNAMCKLFTGLYHJGYFGGIFLFLITDRYLAVH 132

QY 145 AVFALKARTVTFGVVTSWITLVAVFASVPGVLIETKCOKEDESVYVCGYFP --- RGWNW 200
 DB 133 AVFALKARTVTFGVVTSWITLVAVFASVPGVLIETKCOKEDESVYVCGYFP SQYQWKN 192

QY 201 FHTMMRNGLVPLLNVICGILKLLTLLRNEKKAHRVAVTIVMIVFLFWPYN 260
 DB 193 FQFLKTVIGLVLPLLYMVICGILKLLTLLRNEKKAHRVAVTIVMIVFLFWPYN 252

QY 261 IVVLLNTQFQEFFGLNSCNESTSQLDQATOVTETLGTMHCINPITYAFGEKFRSLF --- 316
 DB 253 IVVLLNTQFQEFFGLNSCNESTSQLDQATOVTETLGTMHCINPITYAFGEKFRNLWFF 312

QY 317 --HIA 319
 DB 313 QKHTA 317

RESULT 8

CKR5_MACMU
 ID CKR5_MACMU
 AC P79436; 0027476;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CCR5 OR CMKBR5.
 GN C
 OS Macaca mulatta (Rhesus macaque) (cynomolgus monkey), and
 Macaca fascicularis (Crab eating macaque) (cynomolgus monkey), and
 Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 NCBI_TaxID=9544, 9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta;
 RX MEDLINE=9718452; PubMed=9032394;
 RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
 RA Newman W., Gerard N., Gerard C., Sodroski J.J.;
 RT "Utilization of C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) by the envelope virus,
 RT glycoproteins of a pathogenic simian immunodeficiency virus,
 RT SIVmac239⁺".
 RL [2].
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9721394; PubMed=9060523;
 RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
 RT "Genetically divergent strains of simian immunodeficiency virus use
 RT CCR5 as a coreceptor for entry.";
 RL J. Virol. 71:2705-2714 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta;
 RX MEDLINE=21354164; PubMed=11461684;
 RA Margalites B.J., Hauer D.A., Clements J.B.; rhesus macaque chemokine
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
 RX MEDLINE=97268687; PubMed=108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).

CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC DR EMBL; U71672; AAC51109_1;
 CC DR EMBL; U73139; AAC51158_1;
 CC DR EMBL; U96765; AAC34132_1;
 CC DR EMBL; AF005661; AAB62554_1;
 CC DR EMBL; AF005661; AAB62555_1;
 CC DR EMBL; AF005662; AAB62556_1;
 CC DR InterPro; IPR00276; GPCR_Rhoopsn.
 CC DR Pfam; PF00001; 7tm_1; 1.
 CC DR PRINTS; PRO0237; G_CRRHODOPSIN.
 CC DR PROSITE; PS00232; G_Protein_RICEP_F1_1;
 CC DR PROSITE; PS50282; G_Protein_RICEP_F1_2;
 CC DR G_protein_coupled_receptor; Glycoprotein; Sulfation.
 CC FT DOMAIN 1 30
 CC FT TRANSEM 31 58
 CC FT DOMAIN 59 68
 CC FT TRANSEM 69 89
 CC FT DOMAIN 90 102
 CC FT TRANSEM 103 124
 CC FT DOMAIN 125 141
 CC FT TRANSEM 142 166
 CC FT DOMAIN 167 198
 CC FT TRANSEM 199 218
 CC FT DOMAIN 219 235
 CC FT TRANSEM 236 260
 CC FT DOMAIN 261 277
 CC FT TRANSEM 278 301
 CC FT DOMAIN 302 352
 CC FT DISULFID 101 178
 CC FT MOD_RES 3 3
 CC FT MOD_RES 10 10
 CC FT MOD_RES 14 14
 CC FT MOD_RES 15 15
 CC FT CARBOHYD 268 268
 CC FT N-LINKED (GLCNAC- .) (POTENTIAL).
 CC FT CONFLICT 241 241
 CC FT CONFLICT 292 292
 CC SQ SEQUENCE 352 AA; 40507 MW; 58B96685909FACB2
 CC Query Match 62.4%; Score 1230; DB 1;
 CC Best Local Similarity 76.9%; Pred. No. 1..6e-69;
 CC Matches 237; Conservative 26; Mismatches 33; Indels 12; Gaps 3;

QY 24 FDYD -GAPCHFDYDQGAGLPLPPLYSSVYVGLFTKQKEDSVYVCGYFP --- RG 197
 DB 10 YDIDYTTSEPOKINVQIAARLPLPPLSIVFGVNTVWVAVFSLPLGIFLTGTYCCTSHPYQSQYF 189
 QY 82 LNLAIISDPLFLITPLWAHSANENVFGNAMCKLFTGLYHJGYFGGIFFLITLTIDRYLA 141
 DB 70 LNLAIISDPLFLITPLWAHSANENVFGNAMCKLFTGLYHJGYFGGIFFLITLTIDRYLA 129
 QY 142 IVHAVEALKARTVTFGVVTSWITLVAVFASVPGVLIETKCOKEDESVYVCGYFP --- RG 197
 DB 10 YDIDYTTSEPOKINVQIAARLPLPPLSIVFGVNTVWVAVFSLPLGIFLTGTYCCTSHPYQSQYF 189
 QY 198 WNNFHHTMRNLLGVLPLLINVIVCYSGILKLLRCRNEKKHRARVIFTMIVYFLWT 257
 DB 190 WKNFOILKMWVLLGVLPLLVMWVYCISGILKLLRCRNEKKHRARVIFTMIVYFLWT 249

FT	TRANSMEM	201	220	5 (POTENTIAL).	CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
FT	TRANSMEM	221	237	CYTOSMIC (POTENTIAL).	CC
FT	TRANSMEM	238	262	6 (POTENTIAL).	CC
FT	TRANSMEM	263	279	7 (POTENTIAL).	CC
FT	TRANSMEM	280	303	CYTOSMIC (POTENTIAL).	CC
FT	TRANSMEM	304	354	CYTOSMIC (POTENTIAL).	CC
FT	DISULFID	103	180	BY SIMILARITY.	CC
FT	CARBHYD	270	270	N-LINED (GLCNAC-).	CC
SEQ	SEQUENCE	354	AA:	41030 MW; 77EB368AA4C865D CRC64;	CC
Query Match		62.4%	Score 1230; DB 1; Length 354;		CC
Best Local Similarity		75.0%	Pred: No. 1.6e-59;		CC
Matches	231;	Conservative	29;	Mismatches 42;	CC
				Indels 6;	CC
				Gaps 2;	CC
Qy	17	GEEVTTFFDYY--GAPCHKFDVKOIGAQLPPLPLSVEFEGFVNMLVYLILINCKLK 74			CC
Db	5	GSIPTYIYDDYSMSAPCQVNKOIAQQLPPLPLSVEFEGFVNMMVFLILISCKKLK 64			CC
Qy	75	CLTDIYLNIAISDILFLLTPLWAHSAANNEWVFGNAMCKLFTGLYHIGYFGGIFTILL 134			CC
Db	65	SMTDIYLNIAISDILFLLTPLWAHAYAANNEWVFGNIMCKLFTGLYHIGYFGGIFTILL 124			CC
Qy	135	TIDYLAIVHAFAALKARTVTFGVVTSVITWLAVFASVGIIITFKQEDSVYVCGPYF 194			CC
Db	125	TIDYLAIVHAFAALKARTVTFGVVTSVITWLAVFASVGIIITFKQEDSVYVCGPYF 184			CC
Qy	195	--> PRGWNNFHFTMRNGLVPLPLIMIVCGILKTLLRCRNEKKHRAVRFITIMI 250			CC
Db	185	LHQYRFWKHFQTLKMKVLLSILPLLVWVTCYSGILNLTFCRNEKKHRAVRFITIMI 244			CC
Qy	251	YVFLFWTPYNTVIVLNTFOEFFGLSNCESTSOLDQATOVYETLGMTMHCCTINPIYAYFGE 310			CC
Db	245	YVFLFWTPYNTVIVLNTFOEFFGLSNCESTSOLDQATOVYETLGMTMHCCTINPIYAYFGE 304			CC
Qy	311	KPFSLFH1 318			CC
Db	305	KFRNLYSV 312			CC
Query Match		62.3%	Score 1228; DB 1; Length 352;		CC
Best Local Similarity		76.9%	Pred: No. 2.1e-69;		CC
Matches	237;	Conservative	25;	Mismatches 34;	CC
				Indels 12;	CC
				Gaps 3;	CC
Qy	24	FDYDY--GAPCHKFDVKOIGAQLPPLPLSVEFEGFVNMLVYLILINCKLKCLTDIYL 81			CC
Db	10	YDIDYTFSEPCOKTNQIAARLPLPLSVEFEGFVNMLVYLILINCKLKSMTDIYL 69			CC
Qy	82	LNLAIASDILFLLTPLWAHSAANNEWVFGNAMCKLFTGLYHIGYFGGIFTILLTDRYLA 141			CC
Db	70	LNLAIASDILFLLTPLWAHSAANNEWVFGNAMCKLFTGLYHIGYFGGIFTILLTDRYLA 129			CC
Qy	142	IWHAVFALKARTVTFGVVTSVITWLAVFASVGIIITFKQEDSVYVCGPYF--RG 197			CC
Db	130	IWHAVFALKARTVTFGVVTSVITWLAVFASVGIIITFKQEDSVYVCGPYF--RG 197			CC
Qy	198	WNWFHFTMRNGLVPLPLIMIVCGILKTLLRCRNEKKHRAVRFITIMIYFLWT 257			CC
Db	190	WKNFQFLKTVLQFLVPLLVWVTCYSGILNLTFCRNEKKHRAVRFITIMIYFLWT 249			CC
Qy	258	PYNIVLNTNFOEFFGLSNCESTSOLDQATOVYETLGMTMHCCTINPIYAYFGEKERSLF- 316			CC
Db	250	PYNIVLNTNFOEFFGLSNCESTSOLDQATOVYETLGMTMHCCTINPIYAYFGEKERSLF- 309			CC
Qy	317	----HIA 319			CC
Db	310	VFFQRHIA 317			CC
RESULT	13	CKRS_GORGO	STANDARD;	PRT; 352 AA.	CC
ID	CKRS_GORGO				CC
AC	P56439;				CC
DT	15-JUL-1998	(Rel. 36, Created)			CC
DT	15-JUL-1998	(Rel. 36, Last sequence update)			CC
DT	16-OCT-2001	(Rel. 40, Last annotation update)			CC
DE	CCRS OR CMKRS	Chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR5).			CC
GN		Differential utilization of CCRs by macrophage and T cell tropic simian immunodeficiency virus strains."			CC
RA	Peiper, S.C., Parmentier M., Broder C.C., Doms R.W.,	Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).			CC
RA		MIP-1->BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.			CC
CC		Integral membrane protein.			CC
CC		Belongs to family 1 of G-PROTEIN COUPLED RECEPTORS.			CC
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way			CC
CC		CCRS OR CMKRS.			CC
CC		Papio hamadryas (Hamadryas baboon), and Papio anubis (Olive baboon).			CC

RP	SEQUENCE FROM N.A.	CC	-1- PTM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED GLYCOSYLATION.
RA	McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dediha N., Ansari A., Mardis E., Schutze K., Gnoj L., La Bastide M., Kaplan N., Greco T., Touchman J., Murny D., Chen C.N., Evans C., Fitzgerald J., Pae A., Powell E., Tang M., Porcelli B.M., Dragan Y., Giacalone J., Diaz-Perez S., Zhou X., Yu Y., Solinski K.A., Desilva U., Garcia D., Sagripanti J.L.; Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.	CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
RA		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RL		CC	
RN	SEQUENCE FROM N.A.	CC	
RX	MEDLINE=98001387; PubMed=9343222;	DR	EMBL; X91492; CAA62796.1;
RA	Kutman S.E., Platt E.J., Rozak S.L., Kabat D.; RT	DR	EMBL; U54944; AAC30598.1;
RT	"Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses."	DR	EMBL; U57840; AAC87071.1;
RL	[6]	DR	EMBL; U59626; AAC857793.1;
RN	SEQUENCE FROM N.A., AND POLYMORPHISMS.	DR	EMBL; U83326; AAC85797.1;
RP	MEDLINE=98022612; PubMed=9350654;	DR	EMBL; AF011500; AAC865700.1;
RT	Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., Ho D.D.; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).	DR	EMBL; AF011501; AAC865701.1;
RN	[7]	DR	EMBL; AF011502; AAC865702.1;
RN	SEQUENCE FROM N.A.	DR	EMBL; AF011503; AAC865703.1;
RX	Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.; RT	DR	EMBL; AF011504; AAC865704.1;
RT	"The human CC chemokine receptor 5 (CCR5) gene: Multiple transcripts with 5'-end heterogeneity, dual promoter usage, and evidence for polymorphisms within the regulatory regions and noncoding exons."	DR	EMBL; AF011505; AAC865705.1;
RL	[8]	DR	EMBL; AF011506; AAC865706.1;
RN	SEQUENCE FROM N.A., AND VARIANT ARG-178.	DR	EMBL; AF011507; AAC865707.1;
RA	Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I., Debre P.; Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.	DR	EMBL; AF011508; AAC865708.1;
RP	MEDLINE=96260017; PubMed=8649511;	DR	EMBL; AF011509; AAC865709.1;
RA	Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhardt M., di Marzo P., Marmon S., Hill C.M., Davis C.B., Peiper S.C., Schall T.J., Littman D.R., Landau N.R.; Paxton W.A.; RT	DR	EMBL; AF011510; AAC865710.1;
RA	"Identification of a major co-receptor for primary isolates of HIV-1"; Nature 381:661-666(1996).	DR	EMBL; AF011511; AAC865711.1;
RL	[10]	DR	EMBL; AF011512; AAC865712.1;
RN	CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.	DR	EMBL; AF011513; AAC865713.1;
RP	MEDLINE=96260018; PubMed=8649512;	DR	EMBL; AF011514; AAC865714.1;
RA	Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y., Nagashima K.A., Cayahan C., Maddon P.J., Koup R.A., Moore J.P., Paxton W.A.; RT	DR	EMBL; AF011515; AAC865715.1;
RA	"HIV-1 entry into CD4+ cells is mediated by the chemokine receptor CC-CCR5"; Nature 381:667-673(1996).	DR	EMBL; AF011516; AAC865716.1;
RL	[11]	DR	EMBL; AF011517; AAC865717.1;
RN	SULFATION.	DR	EMBL; AF011518; AAC865718.1;
RP	MEDLINE=99189752; PubMed=10089882;	DR	EMBL; AF011519; AAC865719.1;
RA	Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M., Gerard N.P., Gerard C., Sodroski J., Choe H.; RT	DR	EMBL; AF011520; AAC865720.1;
RA	"Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1 entry"; RT	DR	EMBL; AF011521; AAC865721.1;
RA	Cell 96:667-676(1999).	DR	EMBL; AF011522; AAC865722.1;
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDICES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL, MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-SYNCYTIUM-1-INDUCING STRAINS (NS1) (MACROPHAGE-TROPIC) OF HIV-1 VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.	DR	EMBL; AF011523; AAC865723.1;
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.	DR	EMBL; AF011524; AAC865724.1;
CC	-1- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.	DR	EMBL; AF011525; AAC865725.1;
CC	-1- PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.	DR	EMBL; AF011526; AAC865726.1;
RP		DR	EMBL; AF011527; AAC865727.1;
RN		DR	EMBL; AF011528; AAC865728.1;
RN	CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.	DR	EMBL; AF011529; AAC865729.1;
RP	MEDLINE=96260018; PubMed=8649512;	DR	EMBL; AF011530; AAC865730.1;
RA	Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y., Nagashima K.A., Cayahan C., Maddon P.J., Koup R.A., Moore J.P., Paxton W.A.; RT	DR	EMBL; AF011531; AAC865731.1;
RA	"HIV-1 entry into CD4+ cells is mediated by the chemokine receptor CC-CCR5"; Nature 381:667-673(1996).	DR	EMBL; AF011532; AAC865732.1;
RL	[11]	DR	EMBL; AF011533; AAC865733.1;
RN	SULFATION.	DR	EMBL; AF011534; AAC865734.1;
RP	MEDLINE=99189752; PubMed=10089882;	DR	EMBL; AF011535; AAC865735.1;
RA	Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M., Gerard N.P., Gerard C., Sodroski J., Choe H.; RT	DR	EMBL; AF011536; AAC865736.1;
RA	"Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1 entry"; RT	DR	EMBL; AF011537; AAC865737.1;
RA	Cell 96:667-676(1999).	DR	EMBL; AF031237; AAC894735.1;
RP		DR	EMBL; AF052539; AAC818131.1;
RN		DR	Genew, HGNC:1606; CCR5.
RN		DR	MM, 601373;
RN		DR	InterPro, IPR00276; GPCR_Rhodopsn.
RN		DR	Prints, PF00001; 7tm_1; 1.
RN		DR	Prints, PRO0237; GPCRRODOPSN.
RN		DR	Prosite, PS00237; G-PROTEIN_RECEP_F1-1; 1.
RN		DR	Prosite, PS50262; G-PROTEIN_RECEP_F1-2; 1.
RN		KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Polymorphism.
RN		KW	EXTRACELLULAR (POTENTIAL).
RN		FT	DOMAIN 1 30
RN		FT	TRANSMEM 31 58 1 (POTENTIAL).
RN		FT	DOMAIN 59 68 2 (POTENTIAL).
RN		FT	TRANSMEM 69 89 2 (POTENTIAL).
RN		FT	DOMAIN 90 102 3 (POTENTIAL).
RN		FT	TRANSMEM 103 124 4 (POTENTIAL).
RN		FT	DOMAIN 125 141 4 (POTENTIAL).
RN		FT	TRANSMEM 142 166

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC or send an email to license@isb-sib.ch).

CC EMBL: AAF75448; AA019860; 1;
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
CC G-protein coupled receptor; transmembrane; Glycoprotein; Sulfation.

CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS05082; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; transmembrane; Glycoprotein; Sulfation.

CC FT DOMAIN 10 10 SULFATION.
CC FT DOMAIN 14 14 SULFATION.
CC FT DOMAIN 15 15 SULFATION.
CC FT VARIANT 10 10 Y->D (IN INCCR5-71A).
CC /FTid=VAR_003481.
CC /FTid=d=VAR_011839.
CC R->H (IN INCCR5-72A).

Query Match 62.1%; Score 1224; DB 1; Length 352;
Best Local Similarity 76.3%; Pred. No. 3.8e-69;
Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYDY--GAPCHKEFDVKOIGAQLPPLSVLFEGVNMLVYLINCKKLKCLTDYL 81
Db 10 YDINYYTSPBCQKINVKAARLPLPSLVLFEGVNMLVYLINCKRLKSMTDYL 69

QY 82 LNLAISDLFLITPLWHAASANNEWFGNAMCKLFTGLYHIGYEGGIFPILLTIDRYLA 141
Db 70 LNLAISDLFLITPLWHAASANNEWFGNAMCKLFTGLYHIGYEGGIFPILLTIDRYLA 129

QY 142 IVHAFALKARTVFGVTSVITLWVAVASVPGLITFKCQKEDSVYCGPYFP---RG 197
Db 130 VVHAFALKARTVFGVTSVITLWVAVASLPGITFTPSQEGLHYTSSHFYPSQOF 189

QY 198 WNNFTIMNMLGVLPLMLIVMIVYCGIILKTRCRNEKKRRAVRLIFTIMIVYFLFWT 257
Db 190 WKNFOTLKVIVLGLVPLMLIVMIVYCGIILKTRCRNEKKRRAVRLIFTIMIVYFLFWA 249

QY 258 PYNIVTLNTEQEFGLNSCESTSQLDQATOVTETLGMTCCINPLIYAFVGKEFRSLF- 316
Db 250 PYNIVTLNTEQEFGLNSCESTSQLDQATOVTETLGMTCCINPLIYAFVGKEFRNYLL 309

QY 317 ---HTA 319
Db 310 VFFQKHA 317

RESULT 15
CKR5_PIGNE STANDARD; PRT; 352 AA.
AC 097882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR5).
GN CRKBR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Primates; Catarrhini; Cercopithecidæ; Colobinae;
OC Pygathrix.
OX NCBI_TAXID=54133;
RN SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154 (1999).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA, AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL, MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

Query Match 62.1%; Score 1224; DB 1; Length 352;
Best Local Similarity 76.3%; Pred. No. 3.8e-69;
Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYDY--GAPCHKEFDVKOIGAQLPPLSVLFEGVNMLVYLINCKKLKCLTDYL 81
Db 10 YDIDYTSEPCOKVNTQIAARLPLPSLVLFEGVNMLVYLINCKRLKSMTDYL 69

QY 82 LNLAISDLFLITPLWHAASANNEWFGNAMCKLFTGLYHIGYEGGIFPILLTIDRYLA 141
Db 70 LNLAISDLFLITPLWHAASANNEWFGNAMCKLFTGLYHIGYEGGIFPILLTIDRYLA 129

QY 142 IVHAFALKARTVFGVTSVITLWVAVASVPGLITFKCQKEDSVYCGPYFP---RG 197
Db 130 VVHAFALKARTVFGVTSVITLWVAVASLPGITFTPSQEGLHYTSSHFYPSQOF 189

QY 198 WNNFTIMNMLGVLPLMLIVMIVYCGIILKTRCRNEKKRRAVRLIFTIMIVYFLFWT 257
Db 130 IVHAFALKARTVFGVTSVITLWVAVASLPGITFTPSQEGLHYTSSHFYPSQOF 189

QY 198 WNNFTIMNMLGVLPLMLIVMIVYCGIILKTRCRNEKKRRAVRLIFTIMIVYFLWT 257
Db 190 WNFQTKIVLGLVPLMLIVMIVYCGIILKTRCRNEKKRRAVRLIFTIMIVYFLWA 249

QY 258 PYNIVTLNTEQEFGLNSCESTSQLDQATOVTETLGMTCCINPLIYAFVGKEFRSLF- 316
Db 250 PYNIVTLNTEQEFGLNSCESTSQLDQATOVTETLGMTCCINPLIYAFVGKEFRNYLL 309

QY 317 ---HTA 319
Db 310 VFFQKHA 317

Query Match 62.1%; Score 1224; DB 1; Length 352;
Best Local Similarity 76.3%; Pred. No. 3.8e-69;
Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYDY--GAPCHKEFDVKOIGAQLPPLSVLFEGVNMLVYLINCKKLKCLTDYL 81
Db 10 YDIDYTSEPCOKVNTQIAARLPLPSLVLFEGVNMLVYLINCKRLKSMTDYL 69

QY 82 LNLAISDLFLITPLWHAASANNEWFGNAMCKLFTGLYHIGYEGGIFPILLTIDRYLA 141
Db 70 LNLAISDLFLITPLWHAASANNEWFGNAMCKLFTGLYHIGYEGGIFPILLTIDRYLA 129

QY 142 IVHAFALKARTVFGVTSVITLWVAVASVPGLITFKCQKEDSVYCGPYFP---RG 197
Db 130 IVHAFALKARTVFGVTSVITLWVAVASLPGITFTPSQEGLHYTSSHFYPSQOF 189

QY 198 WNNFTIMNMLGVLPLMLIVMIVYCGIILKTRCRNEKKRRAVRLIFTIMIVYFLWT 257
Db 190 WNFQTKIVLGLVPLMLIVMIVYCGIILKTRCRNEKKRRAVRLIFTIMIVYFLWA 249

QY 258 PYNIVTLNTEQEFGLNSCESTSQLDQATOVTETLGMTCCINPLIYAFVGKEFRSLF- 316
Db 250 PYNIVTLNTEQEFGLNSCESTSQLDQATOVTETLGMTCCINPLIYAFVGKEFRNYLL 309

QY 317 ---HTA 319
Db 310 VFFQKHA 317

